


```

QY 117 SSKATPPSVYPLAPCGDGTGSSVTLGCLVKGFEPESTVTWNSGSLSSVHTFPALIQ 176
|:|||||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 112 SNAKTPPSPVYPLAPSAAGTNSMTVLGCLVKGFEPEPTVTWNSGSLSSVHTFPALIQ 171
QY 177 SGLYTWSSSVYVPSSTWSPSQVTCVAHPASSTVDKLEPSGPISITINPCPKCKHC 236
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 172 SLYLTSSSVYVPSSTWSPSETVTCVAHPASSTYKVDKITYP-----RDC-GCKPC-IC 222
QY 237 PAPNLEGGSVFPEPPNIDVIMLSLTPKTCVYVDSDDDPVOYSMPVNNVEYTAQT 296
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 223 TYPEVS---SVLEFPKPKYDVLITLTPKTCVYVDSKDDPEVQFSWFVDVEYHTAQT 279
QY 297 QTHREDYNSTIRVSTLPIQHODMWSGKEFEKCKVNNKDLPSPIERTISKIKGLVAPQY 356
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 280 QPREDFNSTPFSVSELPIMHODMLNGKEFKCRVNSAARPALEKTIKTKGKAPQY 339
QY 357 ILPPPAQLSRDVSITLCLVGFNPQDISVEWTSNGHTEENYKDTAPVLDSDGYIYK 416
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 340 TTPPEKQAKDKVSLTLCMITDFEPEDITVEWQMGAPENYKNTQPIMDTGSYFYVK 399
QY 417 LNMKTSKWEKTSFSCNVRHEGLKNYLEKKTISRSPK 454
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 400 LNVQKSNMDEAGNTFTCSVLHGLNHNHTEKNLSHSPK 437

```

RESULT 2

```

Q9NPP6 PRELIMINARY: PRT: 416 AA.
AC Q9NPP6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN NCB1_TaxID=9606;
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Auftray C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
RL "The European Image consortium for integrated Molecular analysis of
human gene transcripts.";
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
KL EMBL; AL38978; CAB9753.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 416 AA; 44786 MW; 8C41708BB8A4687 CRC64;
SQ

```

Query Match 22.4%; Score 543; DB 4; Length 416;
 Best Local Similarity 33.3%; Pred. No. 6.3e-35;
 Matches 143; Conservative 76; Mismatches 162; Indels 48; Gaps 19;

```

QY 42 GSELMIGINIFYGSGISPKFKATLTVDKSSSTAYMELSLTSESAVYVCARRAG 101
|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 2 GKGLKLVKATISSGDTVDYADSVKGRFTYSRDTAKNSLSLQSSSLVEEDTAVYCAR--- 58
QY 102 AVY-EDYWGQGTTLVSSAKTTPPSVYPLAPCGDGT--GSSVTLGCLVKGFEPESTV 157
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 59 TYGDMVGQGTTLVSSASPTSPKVFPLST--DSTPDGNNVVAACLVGFGFPQEPISLV 115
QY 158 TWNSGSLSSSVHTFPALLOSG--LVTWSSSVYVPSSTWSP-SQVTCVAH---PASSTTV 211
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

Db 116 TWSESGQNTANRPPSQDASGLYTTSSQLTLPATQCPDGKSVTCVHKYNTPSQVTV 175
QY 212 DKLEPSGFIITINPCPKCKHCAPAPLKEGSPVFIPPNKIDVIMSLTPKTCVYV 271
Db 176 P-----CVPPPPPC-CH-----PRISLRPALEDLLAS-EANLTCTLT 213
QY 272 DVSDDPDVQISMFNANNVHTAQTQTHREDYNSTIRVSTLPIQHODMWSGKEFEKCKVN 331
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 214 GL-RASGATFTWTPSSGK--SAVQGPPEPDLCCGCVSVSVLPQCAQPNNHGETFTCTAA 270
QY 332 NKDLSPIERTISKIKGLVAPQVILPPPAQLSRKD-VSLTCLVGFNPQDISVEWTS 390
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 271 HPELKPTPLANTIK-SGNTFREPHLPPSEELALNELVTLTCLARGSPKDYLVRLQ 329
QY 391 NGH--TEENYKDTAPVLD-SDG--SYFIYSKLNMTSKWEKTSFSCNVRHEGLKNYLYK 445
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 330 GSOELPREKYLWASRQEPESQGTTFPAVSLIRVAEDMKKDDTSCMVGHALLPLAFIQ 389
QY 446 KTISRSPK 454
|:|:|:|:|
Db 390 KTIDRLAK 398

```

RESULT 3

```

Q9QXF0 PRELIMINARY: PRT: 117 AA.
AC Q9QXF0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN NCB1_TaxID=10090;
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ225171; CAB52236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
SQ

```

Query Match 19.8%; Score 480.5; DB 11; Length 117;
 Best Local Similarity 78.8%; Pred. No. 1.1e-30;
 Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

```

QY 1 EVOLQSGPELVKPGASWISCRISATYFTENTYVMWKOSHGESLEMTGGINPYGGSIF 60
|:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 EVOLQSGPELVKPGASWISCRISATYFTENTYVMWKOSHGESLEMTGGINPYGGSIF 60
QY 61 SPKFKGKATLTVDKSSSTAYMELSLTSEDSAVYVCARRAGAYTYDYWGQGTTLVSS 118
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 NQKFKGKATLTVDKSSSTAYMELSLTSEDSAVYVCARRAGAYTYDYWGQGTTLVSS 117

```

RESULT 4

```

Q9UP60 PRELIMINARY: PRT: 384 AA.
AC Q9UP60:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE SNCT3 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


DR Pfam: PF00047; Ig; 6.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 DR SMART: SM00407; IGc1; 1.
 KW SIGNAL.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.
 SQ SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6D6D CRC64;

Query Match 15.3%; Score 372.5; DB 13; Length 684;
 Best Local Similarity 23.6%; Pred. No. 3.3e-21;
 Matches 130; Conservative 88; Mismatches 205; Indels 129; Gaps 23;

QY 2 VOLOQSGPELVKPGASVMISCRISATYFTEN-YVHW-----VQSHSE- 43
 DB 145 VSLHSAITEQRANRFVOLVCLISGY-YPENIAVSQKQNKRTTSGFATSPVTKSSNDF 203
 QY 44 ---SL-----EWIGGINPYGGSIFSPKFKATLTVD---KSSSTAYMELRSLTSED 90
 DB 204 SCASLAKVPLQEW-----SRGSVYSCQVSHSATSSNQRKEISTSEIAYLADPIYEE 256
 QY 91 ----SAVYVC-----ARRAGAYF-----DY 107
 DB 257 IWIDKSATLICEVLSTVSAGVYVSMVNGKVRNEGQMEPTKMGNOYLITSLRLTSYEE 316
 QY 108 WGGSTLTIVSS-----AKTTPSYVPLAGCGD-ITGSSVTLCGLVKG 149
 DB 317 WQSGVEYTCCKAKQDOSTPVYKTRKARVEPTKPLRLPLPSPEIDOSTSATLTCLIRG 376
 QY 150 YFPESVTVTNWNSG--SLSSSVHPFALLQSL-YTMSSSVTPSPSTWPS-QTVTCVSAHP 205
 DB 377 FYPKVSVSMQKDVSVSANTNFPTALEDLTFSTRSLNLTAVEMKSGAKYCTASHP 436
 QY 206 ASSTVDKLEKPPSPITINCPCKECHKCPADNLEGSPVETFPNIKVIMISLTPK 265
 DB 437 PSOSTVKRVIR-----NOKVDCROT-----DISVSLKPPFEET-WTOQTAT 477
 QY 266 VTCVYVVDSEDDPDVQISWPFANNVEVHTAQOTHREDYNSIRVSTLPIQHOMWSKE 325
 DB 478 IVCEI--VYSLENIKVFQWQVNGVETQNPENWSGSKTYSKLKVASLMDSGTE 535
 QY 326 FKCVNNKDLPSPIERTISKIK-GLVRAPQVYLPPPAEOL-SRKDVSLLTGLVGFNPGD 383
 DB 536 YVCLVESELEPTPKASIRKANSQMPKYYLLHPSTEDIDENSATLKLAINFHPAE 595
 QY 384 ISVEWISNGH-TEENYQDTAPVLDSDGYFLYSKLNMKTSKWEKTDSESCNVREGLKNY 442
 DB 596 IYVGMMANDTLDDSGYRQVDSEKSGSSPFVTDRLRLTAEMWSDTYSCLVGHPSLNRD 655
 QY 443 YLKTISRSPCK 454
 DB 656 LIRST-NKSNCK 666

RESULT 11
 Q9Y298 PRELIMINARY; PRT; 150 AA.
 AC Q9Y298;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ICG VH PROTEIN PRECURSOR (FRAGMENT).
 GN ICG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9832215; PubMed=9657749;
 RA Jacquemin M.G., Vander Elst L.P.L.;
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with

RT Inhibitor."
 RL BLOD 92:496-506(1998).
 CC -I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AJ224083; CAA11829.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW SIGNAL.
 FT SIGNAL 1 19 POTENTIAL.
 FT NON_TER 150 150
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB2802D5 CRC64;

Query Match 15.3%; Score 371.5; DB 4; Length 150;
 Best Local Similarity 56.6%; Pred. No. 5.9e-22;
 Matches 73; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
 QY 1 EVOLQSGPELVKPGASVMISCRISATYFTENTYHWKQSHGESLEWIGINPYGGSIF 60
 DB 20 QVOLVQSGAEVKKPGASVSKVSGYTLTLPVHWQQAQAGKGLWVGSPDPSPGESIT 79
 QY 61 SPKFKATLTVDRSSSTAYMELRSLTSEDSAVYYCARAGAYEDYWGQSTLTIVSSAK 120
 DB 80 AREFGQSYTMADSTDIAYMELSLRSDTAYVYCA-VPPDPAFDIWGQSTMTVSSAS 138
 QY 121 TTPPSVPL 129
 DB 139 TKGPSVPL 147

RESULT 12
 O95978 PRELIMINARY; PRT; 157 AA.
 AC O95978;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE VH1 PROTEIN PRECURSOR (FRAGMENT).
 GN VH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
 RA Bohlen H., Diehl V., Wolf J.;
 RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
 RT patient with mixed cellularity Hodgkin's disease is associated with
 RT somatic mutations within the untranslated regions of rearranged and
 RT class switch recombined Ig genes";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AJ005570; CAA06599.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT NON_TER 157 157
 SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D8B5 CRC64;

Query Match 15.2%; Score 369.5; DB 4; Length 157;
 Best Local Similarity 51.9%; Pred. No. 8.9e-22;
 Matches 70; Conservative 25; Mismatches 35; Indels 5; Gaps 2;
 QY 1 EVOLQSGPELVKPGASVMISCRISATYFTENTYHWKQSHGESLEWIGINPYGGSIF 60

Dd	20	QVOLLVQSGAEIKRGASVKYHCKTSYGVFFSYIYHWYRQDROGQLEMMGGIGGVYSTMC	79
QY	61	SPRKCAKATLVDSKSSATWMLSLTSEDSAVYYCAR--- <td>116</td>	116
Dd	80	AEKQGRITMTIRNTSTTYVMELSLRLEFDPTAVYFCGRGGRMRSGNYN--GHWGQGEVTV	138
QY	117	SSAKTTPSYVPLAP	131
Dd	139	SSSSTKGPVSFPLAP	153

RESULT	13
09GYZ2	
ID	09GYZ2
AC	PRELIMINARY;
DT	PRT; 119 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE	MONOCLONAL ANTI-IDIDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS	Schistosoma japonicum (Blood fluke).
OC	Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
CC	Trematoda; Digenea; Strigeidida; Schistosomatoidae; Schistosomatiidae;
CC	Schistosoma
OX	NCBI_TaxID=6182;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Song X.T., Feng Z.Q., Guan X.H.;
RT	"Amplification, cloning and sequence analysis of the heavy chain
RT	variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT	Schistosoma japonicum.";
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF282622; AAG01452.1; -.
FT	
FT	NON_TER 1
FT	NON_TER 119
SQ	SEQUENCE 119 AA; 13567 MW; BA893873FDE5FA6AB CRC64;

[illegible]

RESULT	14		
09URL92			
ID	09UL92	PRELIMINARY;	PRT; 124 AA.
AC	09UL92;		
DT	01-MAY-2000 (TEMBirel. 13, Created)		
DT	01-MAY-2000 (TEMBirel. 13, Last sequence update)		
DT	01-MAR-2001 (TEMBirel. 16, Last annotation update)		
DE	MIOsin-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)		
OS	Homo sapiens (human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal		
RL	fetuses.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
-	1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLE		

```
CC      DOMAIN.
DR      EMBL: AF035022; AAD56258.1; -.
DR      InterPro: IPR003006; -.
DR      InterPro: IPR003596; -.
DR      Pfam: PF00047; 1g; 1.
DR      SMART: SM00406; 1Gv; 1.
DR      NON_TER 1
FT
FT
FT
NON_TER 124
NON_TER 124
SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
```

[illegible]

	RESULT	13		
	Q9JL85			
ID	Q9JL85	PRELIMINARY;	PRT;	109 AA.
AC	Q9JL85;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	ANTI-MYOSIN IMMUNOGLUTELIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Mus musculus (Mouse).			
OCC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OCC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10930;				
(11)				
RN	SEQUENCE FROM N.A.			
RP	STRAIN-BALB/C;			
RC	Malik S., Liao L., Cunningham M.W., Diamond B.;			
RA	"Characterization of cross-reactive monoclonal anti-myosin/anti-n-			
RT	acetyl-glucoamine antibodies from mice with autoimmune myocarditis."			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF206021; AAF69319.1; -			
DR	InterPro: IPR003006; -			
DR	InterPro: IPR003596; -			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
FT	NON_TER	1		
FT	NON_TER	109	109	
SEQUENCE	109 AA; 11944 MW; DFE615FE6CDD4EDE_CRC64;			

Query Match	14.08%	Score 358.5	DB 117	Length 103
Best Local Similarity	63.3%	Pred. 4.1e-21		
Matches	69	Conservative	13	Mismatches 26; Indels 1; Gaps 1;

QY	10	ELVKKPQASWISCRITAYFTTENTYHVMWKOSHESLEWIGINDYGGSIFFPKFGKAT	69
		: : : : : : : : : : : : : : :	
		: : : : : : : : : : : : : : :	
Ddb	2	ELVKKPQASVYKLTSTAGSFNEDITYHMHWKQRPQGLGEMIRIDPATGSHKXDPKFGKAT	61

QY	70	LIVYDKSSATYMLERLSTEDSAVYYICARAGAYIPDYWGQGTLLVYSS	118
		: : : : : : : : : : : : : : :	
		: : : : : : : : : : : : : : :	
Ddb	62	ITSDTSSNATYIQLSITSEDTAYVYCVRR-GAVVEYDWGQGTALTVSS	109

